

From: [Jay Field](#)
To: [Eric Blischke/R10/USEPA/US@EPA](#)
Cc: [Burt Shephard/R10/USEPA/US@EPA](#); Robert.Neely@noaa.gov; [Jay Field](#)
Subject: Re: Logistic Regression Model
Date: 07/14/2008 10:15 AM

Eric,
The LRM approach that I used was based on the combined HY growth & survival endpoint (the lowest of the control-adjusted values for HY growth and survival). The screening step for each individual model run for each chemical excluded from the regression samples classified as hits if the concentration was less than the screening concentration for each study. All no-hit samples and hit samples exceeding the screening concentration were included in the regression for each chemical. All samples, including the samples screened for each individual chemical regression model, were used in the final calibration of the model to the Portland Harbor dataset. Note that several approaches to the screening were used, resulting in several individual models for each chemical. The best performing models for each chemical were selected to be included in the combined (PMax) model.

Does that help or make it more confusing? I'm around all week if you want further explanation.

Jay

Blischke.Eric@epamail.epa.gov wrote:
> Jay, John Toll made the following statement in a conversation last week
> regarding the use of the Hyalella growth endpoint in the logistic
> regression model - The logistic regression model takes the average
> concentration of the no-hit distribution for Hyalella growth, excludes
> samples that with hits above this concentration and then performs the
> regression analysis. Is this accurate? I may not be wording this
> correctly but perhaps you could provide some illumination.
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> Burt, did I get this right?
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> Thanks, Eric
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